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Fitness spectrum of randomly recombined viral genomes

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One of the most enduring puzzles in evolutionary biology is why amphimixy is so widespread through living organisms. In fact, on one hand, recombination potentially brings together beneficial mutations but might also break favourable combinations of interacting mutations. Through this observation some very basic questions remain unresolved: In which extent the events of recombination are lethal, deleterious or advantageous? Among the number of exchanged genomic fragments, which are the positions or their size that would have the greatest phenotypic expression?

In order to avoid the effect of natural selection that might remove lethal recombinants, we created *in vitro* several hundreds of artificial and random recombinants. One or several genome segments of various length have been exchanged between *Tomato yellow leaf curl virus* (mild isolate, TYLCV-Mild) and *Tomato Leaf Curl Virus from Mayotte* (ToLCYTV) at random positions, using the technology of L-DNA shuffling® (Proteus Company, Nîmes, France). These two ssDNA viral species belong to the same *Begomovirus* genus. They are closely related and their overall sequence identity is around 82%. In order to characterize both the genotype and phenotype of a large number of these recombinants, and because the parental viruses are not mechanically transmissible, we have cloned viral genomes into a binary vector of *Agrobacterium tumefaciens*. Those constructions enable clones to be infectious when inoculated into plants.

The reproductive capacity being one major component of the viral fitness, we here report the infectivity and the evaluation of viral accumulation into tomato host plants (*var* Monalbo, INRA), for 50 recombinants randomly extracted from the above described collection. The reproductive capacity is characterized using the Q-PCR technique. The correlation deduced from the comparison of genotypes and this phenotypic trait, will provide the first overview of the effect of “random” recombination events on the viral fitness. More specifically, it will provide a glimpse to regions of the genome that are involved in the different adaptation of the TYLCV-Mild and ToLCYTV to tomato.